

Applicant : David A. Wright et al.  
Serial No. : 09/586,106  
Filed : June 2, 2000  
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Attorney's Docket No.: 08411-032001/ISURF 02410-P1

Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application.

Listing of Claims:

Please amend the claims as follows:

1-14. (Cancelled)

15. (Currently amended) ~~The nucleic acid molecule of claim 9, wherein said nucleic acid molecule comprises~~ An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) ~~a sequence having more than 95% identity to the sequence set forth in SEQ ID NO:62;~~

(b) a sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO:63; and

(c) a sequence fully complementary to (a) or (b).

16. (Currently amended) A transformed seed containing a ~~recombination~~ recombinant construct comprising ~~[[a]] the~~ nucleic acid of claim 15.

17. (Currently amended) A transformed plant containing a ~~recombination~~ recombinant construct comprising ~~[[a]] the~~ nucleic acid of claim 15.

18. (Previously presented) The nucleic acid molecule of claim 33, said nucleic acid further comprising a gag coding sequence and an env coding sequence, wherein adenine-thymidine-guanidine is the gag coding sequence start codon.

19-20. (Cancelled)

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21. (Currently amended) The nucleic acid molecule of claim 15, which further comprises at least one nucleic acid sequence which encodes at least one agronomically-significant characteristic.

22. (Previously presented) The nucleic acid molecule of claim 21, wherein the agronomically-significant characteristic is selected from the group consisting of: male sterility; self-incompatibility; foreign organism resistance; improved biosynthetic pathways; environmental tolerance; photosynthetic pathways; and nutrient content.

23. (Previously presented) The nucleic acid molecule of claim 21, wherein the agronomically-significant characteristic is selected from the group consisting of: fruit ripening; oil biosynthesis; pigment biosynthesis; seed formation; starch metabolism; salt tolerance; cold/frost tolerance; drought tolerance; tolerance to anaerobic conditions; protein content; carbohydrate content (including sugars and starches); amino acid content; and fatty acid content.

24. (Cancelled)

25. (Previously presented) The plant of claim 17, which plant is selected from the group consisting of: soybean; maize; sugar cane; beet; tobacco; wheat; barley; poppy; rape; sunflower; alfalfa; sorghum; rose; carnation; gerbera; carrot; tomato; lettuce; chicory; pepper; melon; cabbage; oat; rye; cotton; flax; potato; pine; walnut; citrus; hemp; oak; rice; petunia; orchids; Arabidopsis; broccoli; cauliflower; brussel sprouts; onion; garlic; leek; squash; pumpkin; celery; pea; bean; strawberries; grapes; apples; pears; peaches; banana; palm; cocoa; cucumber; pineapple; apricot; plum; sugar beet; lawn grasses; maple; triticale; safflower; peanut; and olive.

26-27. (Cancelled)

28. (Currently amended) The nucleic acid molecule of claim ~~[[9]]~~ 15, wherein said nucleic acid molecule encodes a polypeptide having ~~[[an]]~~ the amino acid sequence ~~with 100% identity to set forth in~~ SEQ ID NO:63.

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29. (Currently amended) A transformed seed containing a ~~recombination~~ recombinant construct comprising the nucleic acid of claim 28.
30. (Currently amended) A transformed plant containing a ~~recombination~~ recombinant construct comprising the nucleic acid of claim 28.
31. (Currently amended) The nucleic acid molecule of claim 28, wherein a pol coding sequence comprises said nucleic acid.
32. (Currently amended) The nucleic acid molecule of claim 31, said nucleic acid further comprising a gag coding sequence and an env coding sequence, wherein adenine-thymidine-guanidine is the gag coding sequence start codon.
33. (Currently amended) The nucleic acid molecule of claim 15, wherein a pol coding sequence comprises said nucleic acid.
34. (New) The nucleic acid of molecule claim 15, wherein said nucleotide sequence is the sequence set forth in SEQ ID NO:62.